1600

ENTERED

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 4 <110> APPLICANT: Anderson, David J.
 5         Dong, Xinzhong
 6         Zylka, Mark
 7         Simon, Melvin
 8         Han, Sang-kyou
10 <120> TITLE OF INVENTION: PAIN SIGNALING MOLECULES
13 <130> FILE REFERENCE: CALTE.004C1
15 <140> CURRENT APPLICATION NUMBER: US 09/849,869A
16 <141> CURRENT FILING DATE: 2001-05-04
18 <150> PRIOR APPLICATION NUMBER: US 60/222,344
19 <151> PRIOR FILING DATE: 2000-08-01
21 <150> PRIOR APPLICATION NUMBER: US 60/202,027
22 <151> PRIOR FILING DATE: 2000-05-04
24 <150> PRIOR APPLICATION NUMBER: US 09/704,707
25 <151> PRIOR FILING DATE: 2000-11-03
27 <150> PRIOR APPLICATION NUMBER: US 60/285,493
28 <151> PRIOR FILING DATE: 2001-04-19
30 <160> NUMBER OF SEQ ID NOS: 115
32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 1088
36 <212> TYPE: DNA
37 <213> ORGANISM: Mus Musculus
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (115)...(1026)
43 <400> SEQUENCE: 1
44 acagaagcca gagagctaca tccagcaaga ggaatggggg aaagcagcac ctgtgcaggg 60
45 tttctagccc taaacacatc ggcctcgcca acagcaccca caacaactaa tcca atg   117
46                                                               Met
47                                                                 1
49 gac aat acc atc cct gga ggt atc aac atc acg att ctg atc cca aac   165
50 Asp Asn Thr Ile Pro Gly Gly Ile Asn Ile Thr Ile Leu Ile Pro Asn
51             5                  10                  15
53 ttg atg atc atc atc ttc gga ctg gtc ggg ctg aca gga aat ggc att   213
54 Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Thr Gly Asn Gly Ile
55             20                 25                  30
57 gtg ttc tgg ctc ctg ggc ttc tgt ttg cac agg aac gcc ttc tca gtc   261
58 Val Phe Trp Leu Leu Gly Phe Cys Leu His Arg Asn Ala Phe Ser Val
59         35                 40                  45
61 tac atc cta aac tta gct cta gct gac ttc ttc ttc ctc cta ggt cac   309
62 Tyr Ile Leu Asn Leu Ala Leu Ala Asp Phe Phe Phe Leu Leu Gly His
63 50                 55                  60                  65
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65 atc ata gat tcc ata ctg ctt ctt ctc aat gtt ttc tac cca att acc   357
66 Ile Ile Asp Ser Ile Leu Leu Leu Leu Asn Val Phe Tyr Pro Ile Thr
67              70              75              80
69 ttt ctc ttg tgc ttt tac acg atc atg atg gtt ctc tat atc gca ggc   405
70 Phe Leu Leu Cys Phe Tyr Thr Ile Met Met Val Leu Tyr Ile Ala Gly
71          85              90              95
73 ctg agc atg ctc agt gcc atc agc act gag cgc tgc ctg tct gta ctg   453
74 Leu Ser Met Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu
75          100             105             110
77 tgc ccc atc tgg tat cac tgt cac cgc cca gaa cac aca tca act gtc   501
78 Cys Pro Ile Trp Tyr His Cys His Arg Pro Glu His Thr Ser Thr Val
79      115             120             125
81 atg tgt gct gtc atc tgg gtc ctg tcc ctg ttg atc tgc att ctg aat   549
82 Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile Leu Asn
83 130             135             140             145
85 agt tat ttc tgc ggt ttc tta aat acc caa tat aaa aat gaa aat ggg   597
86 Ser Tyr Phe Cys Gly Phe Leu Asn Thr Gln Tyr Lys Asn Glu Asn Gly
87              150             155             160
89 tgt ctg gca ttg aac ttc ttt act gct gca tac ctg atg ttt ttg ttt   645
90 Cys Leu Ala Leu Asn Phe Phe Thr Ala Ala Tyr Leu Met Phe Leu Phe
91          165             170             175
93 gtg gtc ctc tgt ctg tcc agc ctg gct ctg gtg gcc agg ttg ttc tgt   693
94 Val Val Leu Cys Leu Ser Ser Leu Ala Leu Val Ala Arg Leu Phe Cys
95          180             185             190
97 ggt act ggg cag ata aag ctt acc aga ttg tat gta acc att att ctg   741
98 Gly Thr Gly Gln Ile Lys Leu Thr Arg Leu Tyr Val Thr Ile Ile Leu
99      195             200             205
101 agc att ttg gtt ttt ctc ctt tgc gga ttg ccc ttt ggc atc cac tgg   789
102 Ser Ile Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile His Trp
103 210             215             220             225
105 ttt ctg tta ttc aag att aag gat gat ttt cat gta ttt gat ctt gga   837
106 Phe Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Phe Asp Leu Gly
107             230             235             240
109 ttt tat ctg gca tca gtt gtc ctg act gct att aat agc tgt gcc aac   885
110 Phe Tyr Leu Ala Ser Val Val Leu Thr Ala Ile Asn Ser Cys Ala Asn
111         245             250             255
113 ccc atc att tac ttc ttc gtg gga tcc ttc agg cat cgg ttg aag cac   933
114 Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg His Arg Leu Lys His
115         260             265             270
117 cag acc ctc aaa atg gtt ctc cag aat gca ctg caa gac act cct gag   981
118 Gln Thr Leu Lys Met Val Leu Gln Asn Ala Leu Gln Asp Thr Pro Glu
119     275             280             285
121 aca gcc aaa atc atg gtg gag atg tca aga agc aaa tca gag cca       1026
122 Thr Ala Lys Ile Met Val Glu Met Ser Arg Ser Lys Ser Glu Pro
123 290             295             300
125 tgatgaagag cctttgcctg gcccttagaa gtggctttgg ggtgagcatt gccctgctgc 1086
126 ac                                                               1088
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 304
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RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/849,869A**

DATE: 03/20/2003
TIME: 16:08:26

Input Set : **A:\CALTE.004C1(CP1)revised.txt**
Output Set: **N:\CRF4\03202003\I849869A.raw**

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130 <212> TYPE: PRT
131 <213> ORGANISM: Mus Musculus
133 <400> SEQUENCE: 2
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135  1               5                  10                 15
136 Asn Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Thr Gly Asn Gly
137             20                  25                 30
138 Ile Val Phe Trp Leu Leu Gly Phe Cys Leu His Arg Asn Ala Phe Ser
139         35                  40                 45
140 Val Tyr Ile Leu Asn Leu Ala Leu Ala Asp Phe Phe Phe Leu Leu Gly
141     50                  55                 60
142 His Ile Ile Asp Ser Ile Leu Leu Leu Leu Asn Val Phe Tyr Pro Ile
143 65                  70                 75                 80
144 Thr Phe Leu Leu Cys Phe Tyr Thr Ile Met Met Val Leu Tyr Ile Ala
145             85                  90                 95
146 Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val
147             100                 105                110
148 Leu Cys Pro Ile Trp Tyr His Cys His Arg Pro Glu His Thr Ser Thr
149         115                 120                125
150 Val Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile Leu
151     130                 135                140
152 Asn Ser Tyr Phe Cys Gly Phe Leu Asn Thr Gln Tyr Lys Asn Glu Asn
153 145                 150                155                160
154 Gly Cys Leu Ala Leu Asn Phe Phe Thr Ala Ala Tyr Leu Met Phe Leu
155             165                 170                175
156 Phe Val Val Leu Cys Leu Ser Ser Leu Ala Leu Val Ala Arg Leu Phe
157             180                 185                190
158 Cys Gly Thr Gly Gln Ile Lys Leu Thr Arg Leu Tyr Val Thr Ile Ile
159         195                 200                205
160 Leu Ser Ile Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile His
161     210                 215                220
162 Trp Phe Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Phe Asp Leu
163 225                 230                235                240
164 Gly Phe Tyr Leu Ala Ser Val Val Leu Thr Ala Ile Asn Ser Cys Ala
165                 245                 250                255
166 Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg His Arg Leu Lys
167         260                 265                270
168 His Gln Thr Leu Lys Met Val Leu Gln Asn Ala Leu Gln Asp Thr Pro
169         275                 280                285
170 Glu Thr Ala Lys Ile Met Val Glu Met Ser Arg Ser Lys Ser Glu Pro
171     290                 295                300
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 1234
176 <212> TYPE: DNA
177 <213> ORGANISM: Mus musculus
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (137)...(1051)
183 <400> SEQUENCE: 3
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184 tctgtagtga ctgtatcttt ccttctacac aagccagtga gctacatcca acaagaggat 60
185 tggggaaagc aatggtgaag catttcttgc ctttaagacc tcagcctcac caacagcacc 120
186 agtgacaaca aatcca atg gac gaa acc ctc cct gga agt atc aac att agg 172
187                Met Asp Glu Thr Leu Pro Gly Ser Ile Asn Ile Arg
188                 1               5                      10
190 att ctg atc cca aaa ttg atg atc atc atc ttc gga ctg gtc gga ctg  220
191 Ile Leu Ile Pro Lys Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu
192          15                 20                 25
194 atg gga aac gcc att gtg ttc tgg ctc ctg ggc ttc cac ttg cgc aag  268
195 Met Gly Asn Ala Ile Val Phe Trp Leu Leu Gly Phe His Leu Arg Lys
196    · 30                 35                 40
198 aat gac ttc tca ctc tac atc cta aac ttg gcc cgg gct gac ttc ctt  316
199 Asn Asp Phe Ser Leu Tyr Ile Leu Asn Leu Ala Arg Ala Asp Phe Leu
200  45                 50                 55                 60
202 ttc ctc ctc agt agt atc ata gct tcc acc ctg ttt ctt ctc aaa gtt  364
203 Phe Leu Leu Ser Ser Ile Ile Ala Ser Thr Leu Phe Leu Leu Lys Val
204          ·        65                 70                 75
206 tcc tac ctc agc atc atc ttt cac ttg tgc ttt aac acc att atg atg  412
207 Ser Tyr Leu Ser Ile Ile Phe His Leu Cys Phe Asn Thr Ile Met Met
208          80                 85                 90
210 gtt gtc tac atc aca ggg ata agc atg ctc agt gcc atc agc act gag  460
211 Val Val Tyr Ile Thr Gly Ile Ser Met Leu Ser Ala Ile Ser Thr Glu
212          95                100                105
214 tgc tgc ctg tct gtc ctg tgc ccc acc tgg tat cgc tgc cac cgt cca  508
215 Cys Cys Leu Ser Val Leu Cys Pro Thr Trp Tyr Arg Cys His Arg Pro
216      110                115                · 120
218 gta cat aca tca act gtc atg tgt gct gtg atc tgg gtc cta tcc ctg  556
219 Val His Thr Ser Thr Val Met Cys Ala Val Ile Trp Val Leu Ser Leu
220 125                130                135                140
222 ttg atc tgc att ctg aat agc tat ttc tgt gct gtc tta cat acc aga  604
223 Leu Ile Cys Ile Leu Asn Ser Tyr Phe Cys Ala Val Leu His Thr Arg
224              145                150                155
226 tat gat aat gac aat gag tgt ctg gca act aac atc ttt acc gcc tcg  652
227 Tyr Asp Asn Asp Asn Glu Cys Leu Ala Thr Asn Ile Phe Thr Ala Ser
228              160                165                170
230 tac atg ata ttt ttg ctt gtg gtc ctc tgt ctg tcc agc ctg gct ctg  700
231 Tyr Met Ile Phe Leu Leu Val Val Leu Cys Leu Ser Ser Leu Ala Leu
232          175                180                185
234 ctg gcc agg ttg ttc tgt ggc gct ggg cag atg aag ctt acc aga ttt  748
235 Leu Ala Arg Leu Phe Cys Gly Ala Gly Gln Met Lys Leu Thr Arg Phe
236      190                195                200
238 cat gtg acc atc ttg ctg acc ctt ttg gtt ttt ctc ctc tgc ggg ttg  796
239 His Val Thr Ile Leu Leu Thr Leu Leu Val Phe Leu Leu Cys Gly Leu
240 205                210                215                220
242 ccc ttt gtc atc tac tgc atc ctg tta ttc aag att aag gat gat ttc  844
243 Pro Phe Val Ile Tyr Cys Ile Leu Leu Phe Lys Ile Lys Asp Asp Phe
244              225                230                235
246 cat gta tta gat gtt aat ttt tat cta gca tta gaa gtc ctg act gct  892
247 His Val Leu Asp Val Asn Phe Tyr Leu Ala Leu Glu Val Leu Thr Ala
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Input Set : A:\CALTE.004C1(CP1)revised.txt
Output Set: N:\CRF4\03202003\I849869A.raw

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248              240              245              250
250 att aac agc tgt gcc aac ccc atc atc tac ttc ttc gtg ggc tct ttc   940
251 Ile Asn Ser Cys Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
252         255              260              265
254 aga cat cag ttg aag cac cag acc ctc aaa atg gtt ctc cag agt gca   988
255 Arg His Gln Leu Lys His Gln Thr Leu Lys Met Val Leu Gln Ser Ala
256         270              275              280
258 ctg cag gac act cct gag aca gct gaa aac atg gta gag atg tca agt   1036
259 Leu Gln Asp Thr Pro Glu Thr Ala Glu Asn Met Val Glu Met Ser Ser
260 285              290              295              300
262 aac aaa gca gag cct tgatgaagag cctctacctg gacctcagag gtggctttgg   1091
263 Asn Lys Ala Glu Pro
264              305
266 agtgagcact gccctgctgc acttgaccac tgtccactct tctctcagct tactgatttg 1151
267 acatgcctca gtggtccacc aacaacttca acatctctcc actaacttag tttttctacc 1211
268 cctcctgaat aaaagcatta atc                                          1234
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 305
272 <212> TYPE: PRT
273 <213> ORGANISM: Mus musculus
275 <400> SEQUENCE: 4
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277 1                5                10               15
278 Lys Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Met Gly Asn Ala
279             20               25               30
280 Ile Val Phe Trp Leu Leu Gly Phe His Leu Arg Lys Asn Asp Phe Ser
281             35               40               45
282 Leu Tyr Ile Leu Asn Leu Ala Arg Ala Asp Phe Leu Phe Leu Leu Ser
283     50               55               60
284 Ser Ile Ile Ala Ser Thr Leu Phe Leu Leu Lys Val Ser Tyr Leu Ser
285 65               70               75               80
286 Ile Ile Phe His Leu Cys Phe Asn Thr Ile Met Met Val Val Tyr Ile
287             85               90               95
288 Thr Gly Ile Ser Met Leu Ser Ala Ile Ser Thr Glu Cys Cys Leu Ser
289             100              105              110
290 Val Leu Cys Pro Thr Trp Tyr Arg Cys His Arg Pro Val His Thr Ser
291         115              120              125
292 Thr Val Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile
293     130              135              140
294 Leu Asn Ser Tyr Phe Cys Ala Val Leu His Thr Arg Tyr Asp Asn Asp
295 145              150              155              160
296 Asn Glu Cys Leu Ala Thr Asn Ile Phe Thr Ala Ser Tyr Met Ile Phe
297             165              170              175
298 Leu Leu Val Val Leu Cys Leu Ser Ser Leu Ala Leu Leu Ala Arg Leu
299             180              185              190
300 Phe Cys Gly Ala Gly Gln Met Lys Leu Thr Arg Phe His Val Thr Ile
301         195              200              205
302 Leu Leu Thr Leu Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Val Ile
303     210              215              220
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VERIFICATION SUMMARY   DATE: 03/20/2003
PATENT APPLICATION: **US/09/849,869A**   TIME: 16:08:27

Input Set : **A:\CALTE.004C1(CP1)revised.txt**
Output Set: **N:\CRF4\03202003\I849869A.raw**

L:5310 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:5313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:114